

# SEQUENCE LISTING

<110> Meyers, Rachel  
Rudolph-Owen, Laura

<120> 26934, A Novel Cytidine Deaminase-Like  
Molecule and Uses Thereof

<130> 35800/213921

<150> 60/188,294

<151> 2000-03-10

<160> 4

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<210> 1

<211> 1585

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (149)...(1165)

<221> misc\_feature

<222> (1)...(1585)

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gagaggaggt gagaggcggg ggcgctaggg ccgagatcat gtctgactgg gagaggtttc	120
cttggcagca gaggacgcta ggtttggg atg aaa gaa gct ggg cag atg caa	172
Met Lys Glu Ala Gly Gln Met Gln	

1

5

aat ctg gag agc gcg agg gcc ggg cgg tca gtc agc acc cag act ggc	220
Asn Leu Glu Ser Ala Arg Ala Gly Arg Ser Val Ser Thr Gln Thr Gly	
10 15 20	

agc atg acc ggt cag ata cca agg ctt tct aaa gtc aac ctt ttc act	268
Ser Met Thr Gly Gln Ile Pro Arg Leu Ser Lys Val Asn Leu Phe Thr	
25 30 35 40	

ctg ctc agc ctc tgg atg gag ctc ttt cca gca gaa gcc cag cgg caa	316
Leu Leu Ser Leu Trp Met Glu Leu Phe Pro Ala Glu Ala Gln Arg Gln	
45 50 55	

aaa tct cag aaa aat gaa gag gga aag cat gga ccc tta gga gat aat	364
Lys Ser Gln Lys Asn Glu Glu Gly Lys His Gly Pro Leu Gly Asp Asn	
60 65 70	

gaa gag agg acc aga gta tct act gac aaa aga cag gta aag aga act Glu Glu Arg Thr Arg Val Ser Thr Asp Lys Arg Gln Val Lys Arg Thr 75 80 85	412
ggt ctt gtg gtg gtg aaa aac atg aaa att gtt ggt ctc cac tgt tct Gly Leu Val Val Val Lys Asn Met Lys Ile Val Gly Leu His Cys Ser 90 95 100	460
agt gaa gat tta cat gcc ggg cag att gct ctt att aaa cat ggg tca Ser Glu Asp Leu His Ala Gly Gln Ile Ala Leu Ile Lys His Gly Ser 105 110 115 120	508
agg ctg aaa aac tgt gat ctt tat ttt tcc aga aaa cca tgt tct gct Arg Leu Lys Asn Cys Asp Leu Tyr Phe Ser Arg Lys Pro Cys Ser Ala 125 130 135	556
tgt ttg aaa atg att gta aat gct gga gtt aac cga att tca tac tgg Cys Leu Lys Met Ile Val Asn Ala Gly Val Asn Arg Ile Ser Tyr Trp 140 145 150	604
cct gct gat cca gaa ata agt ttg ctt acg gag gct tct agt tct gaa Pro Ala Asp Pro Glu Ile Ser Leu Leu Thr Glu Ala Ser Ser Ser Glu 155 160 165	652
gat gca aag tta gat gcc aaa gca gtg gaa aga ttg aag tca aac agt Asp Ala Lys Leu Asp Ala Lys Ala Val Glu Arg Leu Lys Ser Asn Ser 170 175 180	700
cgg gcc cat gtg tgt gtc tta ctt caa cct ttg gtg tgt tat atg gtg Arg Ala His Val Cys Val Leu Leu Gln Pro Leu Val Cys Tyr Met Val 185 190 195 200	748
cag ttt gta gag gag acc tct tac aaa tgt gac ttt att caa aaa att Gln Phe Val Glu Glu Thr Ser Tyr Lys Cys Asp Phe Ile Gln Lys Ile 205 210 215	796
aca aaa aca ttg ccg gat gct aac act gac ttt tat tat gaa tgt aaa Thr Lys Thr Leu Pro Asp Ala Asn Thr Asp Phe Tyr Tyr Glu Cys Lys 220 225 230	844
caa gaa aga ata aaa gaa tat gaa atg tta ttt ttg gtt tca aat gaa Gln Glu Arg Ile Lys Glu Tyr Glu Met Leu Phe Leu Val Ser Asn Glu 235 240 245	892
gaa atg cat aag caa ata ctg atg act ata ggt ttg gag aac ctg tgt Glu Met His Lys Gln Ile Leu Met Thr Ile Gly Leu Glu Asn Leu Cys 250 255 260	940
gaa aat cca tac ttt agc aat cta agg caa aac atg aaa gac ctt atc Glu Asn Pro Tyr Phe Ser Asn Leu Arg Gln Asn Met Lys Asp Leu Ile 265 270 275 280	988
cta ctt ttg gcc aca gta gct tcc agt gtg ccg aac ttt aaa cac ttc Leu Leu Leu Ala Thr Val Ala Ser Ser Val Pro Asn Phe Lys His Phe 285 290 295	1036

gga ttt tac cgt agc aat cca gaa cag att aat gaa att cac aat caa	1084
Gly Phe Tyr Arg Ser Asn Pro Glu Gln Ile Asn Glu Ile His Asn Gln	
300 305 310	
agt ttg cca cag gaa att gca agg cac tgc atg gtt cag gcc agg tta	1132
Ser Leu Pro Gln Glu Ile Ala Arg His Cys Met Val Gln Ala Arg Leu	
315 320 325	
ttg gca tat cga act ggt gag tta cat aga tcg taaattgggg ctgattgggt	1185
Leu Ala Tyr Arg Thr Gly Glu Leu His Arg Ser	
330 335	
gggttgatt tgtctctgaa gtgttcgtct catttatggt agagttcatt tactcatagt	1245
tacttaagtt ttgctgttca tacaatatag agaagttagt gagacccttg agtagacaac	1305
tctttctccc agcagttttg ggatttccttg tagccttata ttcagtacca catttctaca	1365
tcaggccctc attaatctag gcccttcttt ctgcttcttg cttttatgat ttcactgktc	1425
cttgagccct ccactaaagg taggacaaga agagaaagga gaggccagtc gcagtgggtc	1485
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<210> 2

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2

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Leu Ser Lys Val Asn Leu Phe Thr Leu Leu Ser Leu Trp Met Glu Leu	
35 40 45	
Phe Pro Ala Glu Ala Gln Arg Gln Lys Ser Gln Lys Asn Glu Glu Gly	
50 55 60	
Lys His Gly Pro Leu Gly Asp Asn Glu Glu Arg Thr Arg Val Ser Thr	
65 70 75 80	
Asp Lys Arg Gln Val Lys Arg Thr Gly Leu Val Val Val Lys Asn Met	
85 90 95	
Lys Ile Val Gly Leu His Cys Ser Ser Glu Asp Leu His Ala Gly Gln	
100 105 110	
Ile Ala Leu Ile Lys His Gly Ser Arg Leu Lys Asn Cys Asp Leu Tyr	
115 120 125	
Phe Ser Arg Lys Pro Cys Ser Ala Cys Leu Lys Met Ile Val Asn Ala	
130 135 140	
Gly Val Asn Arg Ile Ser Tyr Trp Pro Ala Asp Pro Glu Ile Ser Leu	
145 150 155 160	
Leu Thr Glu Ala Ser Ser Glu Asp Ala Lys Leu Asp Ala Lys Ala	
165 170 175	
Val Glu Arg Leu Lys Ser Asn Ser Arg Ala His Val Cys Val Leu Leu	
180 185 190	
Gln Pro Leu Val Cys Tyr Met Val Gln Phe Val Glu Glu Thr Ser Tyr	
195 200 205	
Lys Cys Asp Phe Ile Gln Lys Ile Thr Lys Thr Leu Pro Asp Ala Asn	
210 215 220	

Thr Asp Phe Tyr Tyr Glu Cys Lys Gln Glu Arg Ile Lys Glu Tyr Glu  
 225 230 235 240  
 Met Leu Phe Leu Val Ser Asn Glu Glu Met His Lys Gln Ile Leu Met  
 245 250 255  
 Thr Ile Gly Leu Glu Asn Leu Cys Glu Asn Pro Tyr Phe Ser Asn Leu  
 260 265 270  
 Arg Gln Asn Met Lys Asp Leu Ile Leu Leu Ala Thr Val Ala Ser  
 275 280 285  
 Ser Val Pro Asn Phe Lys His Phe Gly Phe Tyr Arg Ser Asn Pro Glu  
 290 295 300  
 Gln Ile Asn Glu Ile His Asn Gln Ser Leu Pro Gln Glu Ile Ala Arg  
 305 310 315 320  
 His Cys Met Val Gln Ala Arg Leu Leu Ala Tyr Arg Thr Gly Glu Leu  
 325 330 335  
 His Arg Ser

<210> 3  
 <211> 1017  
 <212> DNA  
 <213> Homo sapiens

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 ctgctcagcc tctggatgga gctctttcca gcagaagccc agcggcaaaa atctcagaaa 180  
 aatgaagagg gaaagcatgg acccttagga gataatgaag agaggaccag agtatctact 240  
 gacaaaagac aggtaaagag aactggtctt gtggtggtga aaaacatgaa aattggttgt 300  
 ctccactgtt ctagtgaaga ttacatgcc gggcagattg ctcttattaa acatgggtca 360  
 aggctgaaaa actgtgatct ttatttttcc agaaaaccat gttctgcttg tttgaaaatg 420  
 attgtaaatg ctggagttaa ccgaatttca tactggcctg ctgatccaga aataagtttg 480  
 cttacggagg cttctagttc tgaagatgca aagttagatg ccaaagcagt ggaaagattg 540  
 aagtcaaaca gtcgggcccc tgtgtgtgtc ttacttcaac ctttgggtgtg ttatatggtg 600  
 cagtttgtag aggagacctc ttacaaatgt gactttattc aaaaaattac aaaaacattg 660  
 ccggatgcta acactgactt ttattatgaa tgtaaacaag aaagaataaa agaatatgaa 720  
 atgttatttt tggtttcaaa tgaagaaatg cataagcaaa tactgatgac tatagggttg 780  
 gagaacctgt gtgaaaatcc atacttttagc aatctaaggc aaaacatgaa agaccttattc 840  
 ctacttttgg ccacagtagc ttccagtgtg ccgaacttta aacacttcgg attttaccgt 900  
 agcaatccag aacagattaa tgaaattcac aatcaaagtt tgccacagga aattgcaagg 960  
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<210> 4  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PFAM consensus sequence for cytidine and  
 deoxycytidylate deaminase zinc-binding region

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 Gly Arg Ile Phe Gly Val Asn Ser Glu Gly Ala Asn Tyr Val Glu Gly  
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-	35						40					45			
Lys	Ala	Val	Ser	Glu	Arg	Tyr	Arg	Asp	Phe	Lys	Ile	Arg	Leu	Gly	Gly
50						55					60				
Glu	Arg	Leu	Glu	Gly	Ala	Thr	Leu	Tyr	Val	Thr	Leu	Glu	Pro	Cys	Gly
65					70					75					80
His	Tyr	Gly	Arg	Thr	Pro	Met	Cys	Ala	Gln	Ala	Ile	Ile	Glu	Ser	Gly
				85					90					95	
Ile	Lys	Lys	Val												
			100												